



SEQUENCE LISTING

<110> Sunol Molecular Corporatiopn
Sherman, Linda
Lustgarten, Joseph

<120> RECOMBINANT CONSTRUCTS ENCODING T CELL
RECEPTORS SPECIFIC FOR HUMAN HLA-RESTRICTED TUMOR ANTIGENS

<130> 31333-20001.01

<140> US 09/774,681
<141> 2001-02-01

<150> US 08/812,393
<151> 1997-03-05

<150> US 60/012,845
<151> 1996-03-05

<160> 65

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 1350
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<213> Artificial Sequence

<220>
<223> Polynucleotide derivative of effective T cell
receptor

<221> CDS
<222> (1)...(1350)

<400> 1
ctc gag atg cag agg aac ctg gga gct gtg ctg ggg att ctg tgg gtg 48
Leu Glu Met Gln Arg Asn Leu Gly Ala Val Leu Gly Ile Leu Trp Val
1 5 10 15

cag att tgc tgg ctg aaa gaa cag caa gtg cag cag agt ccc gca tcc 96
Gln Ile Cys Trp Leu Lys Glu Gln Val Gln Gln Ser Pro Ala Ser
20 25 30

ttg gtt ctg cag gag ggg gag aac gca gag ctc cag tgt agc ttt tcc 144
Leu Val Leu Gln Glu Gly Glu Asn Ala Glu Leu Gln Cys Ser Phe Ser
35 40 45

atc ttt aca aac cag gtg cag tgg ttt tac caa cgt cct ggg gga aga 192
Ile Phe Thr Asn Gln Val Gln Trp Phe Tyr Gln Arg Pro Gly Gly Arg
50 55 60

ctc gtc agc ctg ttg tac aat cct tct ggg aca aag cag agt ggg aga 240
Leu Val Ser Leu Leu Tyr Asn Pro Ser Gly Thr Lys Gln Ser Gly Arg

65	70	75	80	
ctg aca tcc aca aca gtc att aaa gaa cgt cgc agc tct ttg cac att				288
Leu Thr Ser Thr Thr Val Ile Lys Glu Arg Arg Ser Ser Leu His Ile				
85	90	95		
tcc tcc tcc cag atc aca gac tca ggc act tat ctc tgt gcc tca aat				336
Ser Ser Ser Gln Ile Thr Asp Ser Gly Thr Tyr Leu Cys Ala Ser Asn				
100	105	110		
tct gga gga agc aat gca aag cta acc ttc ggg aaa ggc act aaa ctc				384
Ser Gly Gly Ser Asn Ala Lys Leu Thr Phe Gly Lys Gly Thr Lys Leu				
115	120	125		
tct gtt aaa tca ggt ggc gga ggg tct ggc ggg ggt gga tcc ggg ggt				432
Ser Val Lys Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly				
130	135	140		
gga ggc tca gag gct gca gtc acc caa agc cca aga aac aag gtg gca				480
Gly Gly Ser Glu Ala Ala Val Thr Gln Ser Pro Arg Asn Lys Val Ala				
145	150	155	160	
gta aca gga gga aag gtg aca ttg agc tgt aat cag act aat aac cac				528
Val Thr Gly Gly Lys Val Thr Leu Ser Cys Asn Gln Thr Asn Asn His				
165	170	175		
aac aac atg tac tgg tat cgg cag gac acg ggg cat ggg ctg agg ctg				576
Asn Asn Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu				
180	185	190		
atc cat tat tca tat ggt gct ggc agc act gag aaa gga gat atc cct				624
Ile His Tyr Ser Tyr Gly Ala Gly Ser Thr Glu Lys Gly Asp Ile Pro				
195	200	205		
gat gga tac aag gcc tcc aga cca agc caa gag aac ttc tcc ctc att				672
Asp Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile				
210	215	220		
gtg gag ttg ggt acc ccc tct cag aca tca gtg tac ttc tgt gcc agc				720
Val Glu Leu Gly Thr Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser				
225	230	235	240	
ggt gag aca ggg acc aac gaa aga tta ttt ttc ggt cat gga acc aag				768
Gly Glu Thr Gly Thr Asn Glu Arg Leu Phe Phe Gly His Gly Thr Lys				
245	250	255		
ctg tct gtc ctg act agt aac tcc atc atg tac ttc agc cac ttc gtg				816
Leu Ser Val Leu Thr Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val				
260	265	270		
ccg gtc ttc ctg cca gcg aag ccc acc acg acg cca gcg ccg cga cca				864
Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Pro Ala Pro Arg Pro				
275	280	285		
cca aca ccg gcg ccc acc atc gcg tcg cag ccc ctg tcc ctg cgc cca				912
Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro				
290	295	300		

tct agt tct aga gat ccc aaa ctc tgc tac ctg ctg gat gga atc ctc	960
Ser Ser Ser Arg Asp Pro Lys Leu Cys Tyr Leu Leu Asp Gly Ile Leu	
305 310 315 320	
ttc atc tat ggt gtc att ctc act gcc ttg ttc ctg aga gtg aag ttc	1008
Phe Ile Tyr Gly Val Ile Leu Thr Ala Leu Phe Leu Arg Val Lys Phe	
325 330 335	
agc agg agc gca gac gcc ccc gcg tac cag cag ggc cag aac cag ctc	1056
Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu	
340 345 350	
tat aac gag ctc aat cta gga cga aga gag gag tac gat gtt ttg gac	1104
Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp	
355 360 365	
aag aga cgt ggc cgg gac cct gag atg ggg gga aag ccg aga agg aag	1152
Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys	
370 375 380	
aac cct cag gaa ggc ctg tac aat gaa ctg cag aaa gat aag atg gcg	1200
Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala	
385 390 395 400	
gag gcc tac agt gag att ggg atg aaa ggc gag cgc cgg agg ggc aag	1248
Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys	
405 410 415	
ggg cac gat ggc ctt tac cag ggt ctc agt aca gcc acc aag gac acc	1296
Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr	
420 425 430	
tac gac gcc ctt cac atg cag gcc ctg ccc cct cgc taa gcg gcc gcc	1344
Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg * Ala Ala Ala	
435 440 445	
acc gcg	1350
Thr Ala	

<210> 2
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Deduced amino acid derivative of effective T cell
receptor

<400> 2
Leu Glu Met Gln Arg Asn Leu Gly Ala Val Leu Gly Ile Leu Trp Val
1 5 10 15
Gln Ile Cys Trp Leu Lys Glu Gln Gln Val Gln Gln Ser Pro Ala Ser
20 25 30
Leu Val Leu Gln Glu Gly Glu Asn Ala Glu Leu Gln Cys Ser Phe Ser

35	40	45	
Ile Phe Thr Asn Gln Val Gln Trp Phe Tyr Gln Arg Pro Gly Gly Arg			
50	55	60	
Leu Val Ser Leu Leu Tyr Asn Pro Ser Gly Thr Lys Gln Ser Gly Arg			
65	70	75	
Leu Thr Ser Thr Thr Val Ile Lys Glu Arg Arg Ser Ser Leu His Ile		80	
85	90	95	
Ser Ser Ser Gln Ile Thr Asp Ser Gly Thr Tyr Leu Cys Ala Ser Asn			
100	105	110	
Ser Gly Gly Ser Asn Ala Lys Leu Thr Phe Gly Lys Gly Thr Lys Leu			
115	120	125	
Ser Val Lys Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly			
130	135	140	
Gly Gly Ser Glu Ala Ala Val Thr Gln Ser Pro Arg Asn Lys Val Ala			
145	150	155	160
Val Thr Gly Lys Val Thr Leu Ser Cys Asn Gln Thr Asn Asn His			
165	170	175	
Asn Asn Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu			
180	185	190	
Ile His Tyr Ser Tyr Gly Ala Gly Ser Thr Glu Lys Gly Asp Ile Pro			
195	200	205	
Asp Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile			
210	215	220	
Val Glu Leu Gly Thr Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser			
225	230	235	240
Gly Glu Thr Gly Thr Asn Glu Arg Leu Phe Phe Gly His Gly Thr Lys			
245	250	255	
Leu Ser Val Leu Thr Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val			
260	265	270	
Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Pro Ala Pro Arg Pro			
275	280	285	
Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro			
290	295	300	
Ser Ser Ser Arg Asp Pro Lys Leu Cys Tyr Leu Leu Asp Gly Ile Leu			
305	310	315	320
Phe Ile Tyr Gly Val Ile Leu Thr Ala Leu Phe Leu Arg Val Lys Phe			
325	330	335	
Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu			
340	345	350	
Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp			
355	360	365	
Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys			
370	375	380	
Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala			
385	390	395	400
Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys			
405	410	415	
Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr			
420	425	430	
Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Ala Ala Ala Thr			
435	440	445	
Ala			

<210> 3
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<213> Artificial Sequence

<220>

<223> Primer

<400> 3

cccaaggcac tgatgttcat cttc

24

<210> 4

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 4

tgagacaaag tccccaaatct ctgacag

27

<210> 5

<211> 26

<212> DNA

<213> Primer

<220>

<223> Primer

<400> 5

ctgcagctgc tcctcaagta ctattc

26

<210> 6

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 6

tcccgagaa ggtccacagt tcctcttt

28

<210> 7

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 7

gaagcagcag agggttgaa gccacatac

29

<210> 8

<211> 27

<212> DNA

<213> Artificial Sequence

<220>
<223> Primer

<400> 8
ggcaggctt cagttgctta tgaagg

27

<210> 9
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 9
ggtcctt cagcgtccag aatatgt

27

<210> 10
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 10
gcgaagaact caccctggac tgttcat

27

<210> 11
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 11
gagctccaca gacaacaaga gcaccgagca

30

<210> 12
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 12
gagctgcgac gttccttagt gactgtg

27

<210> 13
<211> 30
<212> DNA
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<220>
<223> Primer

<400> 13
cctcgtcagc ctgttgtcca atccttctgg 30

<210> 14
<211> 28
<212> DNA
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<220>
<223> Primer

<400> 14
cagcctcatc aatctgttct acttggtc 28

<210> 15
<211> 28
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<220>
<223> Primer

<400> 15
ccaccaggga ccacagttt tcattcaa 28

<210> 16
<211> 27
<212> DNA
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<220>
<223> Primer

<400> 16
acctggagac aatcctaagc tcatcat 27

<210> 17
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<220>
<223> Primer

<400> 17
aggtcttgtc tccctgacag tcctggtt 28

<210> 18
<211> 30
<212> DNA
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<220>
<223> Primer

<400> 18

caagcaaaca ctgttagtgca gagcccttcc

30

<210> 19
<211> 25
<212> DNA
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<220>
<223> Primer

<400> 19
caagacatcc ataactgccc tacag

25

<210> 20
<211> 27
<212> DNA
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<220>
<223> Primer

<400> 20
gtgtatgaaa cccaggacag ttcttac

27

<210> 21
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 21
ccgtatctt ttcttatgtt gttttggat

29

<210> 22
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 22
caaagctctc catcgctgac tggcaag

28

<210> 23
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 23
atctaattcct gggaaagagca aat

23

<210> 24
<211> 23
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<220>
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<400> 24
ggcgtctgg accacgtggt caa 23

<210> 25
<211> 23
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<220>
<223> Primer

<400> 25
gtgaaagggc aaggacaaaa agc 23

<210> 26
<211> 22
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<220>
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<400> 26
gatatgcgaa cagtatctag gc 22

<210> 27
<211> 23
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<220>
<223> Primer

<400> 27
acataatcaa aggaaagggg gaa 23

<210> 28
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
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<400> 28
tcctgattgg tcacgaaggg caa 23

<210> 29
<211> 23

<212> DNA
<213> Artificial Sequence

<220>
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<400> 29
tacctgatca aaagaatggg aga

23

<210> 30
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<220>
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<400> 30
ataaccatga caatatgtac tgg

23

<210> 31
<211> 23
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<220>
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<400> 31
ataaccacaa caacatgtac tgg

23

<210> 32
<211> 23
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<220>
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<400> 32
atagccacaa ctacatgtac tgg

23

<210> 33
<211> 23
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<220>
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<400> 33
agcttgcaag agttggaaaa cca

23

<210> 34
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<212> DNA
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<220>
<223> Primer

<400> 34
gattatgttt agctacaata ata 23

<210> 35
<211> 23
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<220>
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<400> 35
acaaggtgac aggaaaggga caa 23

<210> 36
<211> 23
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<213> Artificial Sequence

<220>
<223> Primer

<400> 36
acctacagaa cccaggact cag 23

<210> 37
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 37
cagttgccct cggatcgatt ttc 23

<210> 38
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 38
gccgagatca aggctgtggg cag 23

<210> 39
<211> 23
<212> DNA
<213> Artificial Sequence

<220>

<223> Primer

<400> 39
agaaccatct gtaagagtgg aac

23

<210> 40
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 40
catcaaataa tagatatggg gca

23

<210> 41
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 41
gtagtcctga aaaagggcac act

23

<210> 42
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 42
catctgtcaa agtggcactt ca

22

<210> 43
<211> 393
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of the variable regions of the
alpha chain of H7-specific TCR

<221> CDS
<222> (1) ... (393)

<400> 43
atg aaa tcc ttg agt gtt tcc cta gtg gtc ctg tgg ctc cag tta aac
Met Lys Ser Leu Ser Val Ser Leu Val Val Leu Trp Leu Gln Leu Asn
1 5 10 15

48

tgg gtg cag agc cag cag aag gtg cag cag agc cca gaa tcc ctc agt
Trp Val Gln Ser Gln Gln Lys Val Gln Gln Ser Pro Glu Ser Leu Ser

96

20

25

30

gtc cca gag gga ggc atg gcc tct ctc aac tgc act tca agt gat cgc	144		
Val Pro Glu Gly Gly Met Ala Ser Leu Asn Cys Thr Ser Ser Asp Arg			
35	40	45	
aat ttt cag tat ttc tgg tgg tac aga cag cat tct gga gaa ggc ccc	192		
Asn Phe Gln Tyr Phe Trp Trp Tyr Arg Gln His Ser Gly Glu Gly Pro			
50	55	60	
aaa gca ctg atg tcc atc ttc tct gat ggt gac aag aaa gaa ggc aga	240		
Lys Ala Leu Met Ser Ile Phe Ser Asp Gly Asp Lys Lys Glu Gly Arg			
65	70	75	80
ttc aca gct cac ctc aat aag gcc agc ctg cat gtt tcc ctg cac atc	288		
Phe Thr Ala His Leu Asn Lys Ala Ser Leu His Val Ser Leu His Ile			
85	90	95	
aga gac tcc cag ccc agt gac tcc gct ctc tac ttc tgt gca gtt atg	336		
Arg Asp Ser Gln Pro Ser Asp Ser Ala Leu Tyr Phe Cys Ala Val Met			
100	105	110	
gat tat aac cag ggg aag ctt atc ttt ggg cag ggt acc aag tta tct	384		
Asp Tyr Asn Gln Gly Lys Leu Ile Phe Gly Gln Gly Thr Lys Leu Ser			
115	120	125	
atc aag ccc	393		
Ile Lys Pro			
130			

<210> 44

<211> 131

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of the variable regions of the
alpha chain of H7-specific TCR

<400> 44

Met Lys Ser Leu Ser Val Ser Leu Val Val Leu Trp Leu Gln Leu Asn				
1	5	10	15	
Trp Val Gln Ser Gln Gln Lys Val Gln Gln Ser Pro Glu Ser Leu Ser				
20	25	30		
Val Pro Glu Gly Gly Met Ala Ser Leu Asn Cys Thr Ser Ser Asp Arg				
35	40	45		
Asn Phe Gln Tyr Phe Trp Trp Tyr Arg Gln His Ser Gly Glu Gly Pro				
50	55	60		
Lys Ala Leu Met Ser Ile Phe Ser Asp Gly Asp Lys Lys Glu Gly Arg				
65	70	75	80	
Phe Thr Ala His Leu Asn Lys Ala Ser Leu His Val Ser Leu His Ile				
85	90	95		
Arg Asp Ser Gln Pro Ser Asp Ser Ala Leu Tyr Phe Cys Ala Val Met				
100	105	110		
Asp Tyr Asn Gln Gly Lys Leu Ile Phe Gly Gln Gly Thr Lys Leu Ser				
115	120	125		

Ile Lys Pro
130

<210> 45

<211> 402

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleotide sequence of the variable regions of the
beta chain of H7-specific TCR

<221> CDS

<222> (1) ... (402)

<400> 45

atg ggc tcc aga ctc ttc ttt gtg gtt ttg att ctc ctg tgt gca aaa
Met Gly Ser Arg Leu Phe Phe Val Val Leu Ile Leu Leu Cys Ala Lys
1 5 10 15

48

cac atg gag gct gca gtc acc caa agt cca aga agc aag gtg gca gta
His Met Glu Ala Ala Val Thr Gln Ser Pro Arg Ser Lys Val Ala Val
20 25 30

96

aca gga gga aag gtg aca ttg agc tgt cac cag act aat aac cat gac
Thr Gly Gly Lys Val Thr Leu Ser Cys His Gln Thr Asn Asn His Asp
35 40 45

144

tat atg tac tgg tat cgg cag gac acg ggg cat ggg ctg agg ctg atc
Tyr Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu Ile
50 55 60

192

cat tac tca tat gtc gct gac agc acg gag aaa gga gat atc cct gat
His Tyr Ser Tyr Val Ala Asp Ser Thr Glu Lys Gly Asp Ile Pro Asp
65 70 75 80

240

ggg tac aag gcc tcc aga cca agc caa gag aat ttc tct ctc att ctg
Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile Leu
85 90 95

288

gag ttg gct tcc ctt tct cag tca gct gta tat ttc tgt gcc agc agc
Glu Leu Ala Ser Leu Ser Gln Ser Ala Val Tyr Phe Cys Ala Ser Ser
100 105 110

336

gat ttc gcc ggg aca ggg ggc ttc tat gaa cag tac ttc ggt ccc ggc
Asp Phe Ala Gly Thr Gly Phe Tyr Glu Gln Tyr Phe Gly Pro Gly
115 120 125

384

acc agg ctc acg gtt tct
Thr Arg Leu Thr Val Ser
130

402

<210> 46

<211> 134

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of the variable regions of the
beta chain of H7-specific TCR

<400> 46

Met Gly Ser Arg Leu Phe Phe Val Val Leu Ile Leu Leu Cys Ala Lys
1 5 10 15
His Met Glu Ala Ala Val Thr Gln Ser Pro Arg Ser Lys Val Ala Val
20 25 30
Thr Gly Gly Lys Val Thr Leu Ser Cys His Gln Thr Asn Asn His Asp
35 40 45
Tyr Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu Ile
50 55 60
His Tyr Ser Tyr Val Ala Asp Ser Thr Glu Lys Gly Asp Ile Pro Asp
65 70 75 80
Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile Leu
85 90 95
Glu Leu Ala Ser Leu Ser Gln Ser Ala Val Tyr Phe Cys Ala Ser Ser
100 105 110
Asp Phe Ala Gly Thr Gly Gly Phe Tyr Glu Gln Tyr Phe Gly Pro Gly
115 120 125
Thr Arg Leu Thr Val Ser
130

<210> 47

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized peptide

<400> 47

Lys Ile Phe Gly Ser Leu Ala Phe Leu
1 5

<210> 48

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized peptide

<400> 48

Thr Leu Gln Gly Leu Gly Ile Ser Trp Leu
1 5 10

<210> 49

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized peptide

<400> 49
Val Met Ala Gly Val Gly Ser Pro Tyr Val
1 5 10

<210> 50
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized peptide

<400> 50
Val Leu Gln Gly Leu Pro Arg Glu Tyr Val
1 5 10

<210> 51
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized peptide

<400> 51
His Leu Tyr Gln Gly Gln Gln Trp
1 5

<210> 52
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized peptide

<400> 52
Arg Leu Leu Gln Glu Thr Glu Leu Val
1 5

<210> 53
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized peptide

<400> 53
Lys Ile Pro Val Ala Ile Lys Val Leu
1 5

<210> 54
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthesized peptide

<400> 54

Cys Leu Thr Ser Thr Val Gln Leu Val
1 5

<210> 55

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized peptide

<400> 55

Gln Leu Met Pro Tyr Gly Cys Leu Leu
1 5

<210> 56

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized peptide

<400> 56

Val Leu Val Lys Ser Pro Asn His Val
1 5

<210> 57

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized peptide

<400> 57

Asp Ile Asp Glu Thr Glu Tyr His Ala
1 5

<210> 58

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized peptide

<400> 58

Asp Leu Leu Glu Lys Gly Glu Arg Leu
1 5

<210> 59

<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized peptide

<400> 59
Glu Leu Val Ser Glu Phe Ser Arg Met
1 5

<210> 60
<211> 10
<212> PRT
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